



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ruddy, David A.  
Wolff, Roger K.
- (ii) TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
HEMOCHROMATOSIS GENE
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds, LLP  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: NY  
(E) COUNTRY: USA  
(F) ZIP: 10036-2811
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/852,495  
(B) FILING DATE: 07-MAY-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Poissant, Brian M  
(B) REGISTRATION NUMBER: 28,462  
(C) REFERENCE/DOCKET NUMBER: 8907-0057-999
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-493-4935  
(B) TELEFAX: 650-493-5556  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 235033 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACACACACA CACACACACA CACACACACA CACACAAATG AGGTATATAA AGGGTCTCCT	60
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CTATTTT TAGA TAGCCTTGTC TGAAACAGAG CTGGGACCTG ATGAGTGAAA ATGAGCTCAC	180
CAGAAGAAAA ATCAAACAGG CATTTTCAGAG ATTGAGGCCA AGAAGTTAAA TGTCTTAAAT	240
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ACAGCAGAAG AGGTGAACAG AGGCCAGAGA TGGTCACTGA GTGGGCCCTT AAGTCATGGT	360
AAGGAGTATG GAGAATGAAT TATTGCATGT ATTGAATATG TAGGTGACGT GACTCACAGA	420
TACTTTGGAT TTGTAGAGAT GAAGGAAATG TAGCAAGTGA CACTCTTAGA ATGTTGATTT	480
GAGTAAATGG TAGTGTCAGT TATTGAACTG GGGAGAACTG GAAGGGATAA CAGGCTTAAG	540
GAGCACGTTT ATTCCTGTGT CTTGGAAGTG TTTAGGGTGA AAGACCTATT AGAGTTCTAA	600
ATGGAGATGT CAAGTGAAAA TGTGGCTACA CACATTTGCA TTTCAGAAAA AAGGTCAGGC	660
TGGAGATGTA AAATTGGAAG TTTACTGCAT ATAGATAGTC TTTGGAACCG TAGTATTGAT	720
GAAGCCATTA ATGAGACAGA ACAAAGACTA GGGACCAGAG CCAAGCTCCA AGTTTCTAAA	780
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GGCTCACGCC TGTAATCTCA GCACTTTGGG AGGCTGAGGG CACAGATCAC GAGGTCGGGA	1440
GTTTGAGACC AGCCTGGCCA ATATGGCGAA ACCCTGTCTC TACTAAAAAT ACAAAAATTA	1500
GCTGGGCATG GTGATGTGCT TCTGTGGTCC CAGCTACTCG GGAGGCTGAG GCTGAAGAAT	1560

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GGACATTAAA	GTCAACTCTT	GTGAGGTCTC	AGATGAAAAT	GAGGGACAGG	TTATTGGAAA	1740
CTGTAGAAAT	CACTGTTCTT	GTTACAATGT	GTCAAGAACT	TGGCTGAATT	ACGCTGTAGT	1800
GTTTACTGGA	AAGAACTTAT	AAGCAGTAAA	ACTGGATATT	TACCAGAAGA	GATGTCTAAG	1860
CAAAGTATTG	AAGGTGTGAT	TTAGGTCCTC	CTTACTGCTT	AAAGTGAAAT	GTGAGAGGAA	1920
AGAGCCGAAA	TAAAGAAGGA	ATTTTTAAGC	AAAACACAAT	CAGAACTTGG	AGATTTGGGA	1980
TAGATTTCTC	AATCTATATT	GTAAAAATTG	AGAAAAGTTTT	TCTTGAAGAG	GTATGGTTGA	2040
ACAATGTTTT	CTTTTTCTTT	TTTTTCTTG	GTTTTATTTT	TATTTTTATG	TTTTTTGAGA	2100
CAGGGTCTGG	CTATGTCATC	CAGGCTGGAG	TGCAGTGGCA	CAATCTCAGT	TCAGTGCAAC	2160
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TTTGTCTCTG	GATGAATCAC	ACATTGAGCC	TCACCCGTAA	CCTGATTTAG	ATGATTTTTT	3480
AGATGACACT	TTGAACTTTA	GAATTGATGC	TAGAATGAGT	TAAGACTTTC	AGGGGGCTGT	3540
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CATGCCCCGC	TGGGATGGAA	TAAATTTATC	TTGTATGGGA	GAAGGACATA	CATTTTGGCA	3900
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATACA	AACACACAGT	GAGATGGCAG	4140
CCATCTGTTA	GCCAGGAACA	GATTCTCACC	ATAAACTATG	TTGGCACCTT	GATCTTAAAC	4200
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GCTAAGACAA	TGAAGGATGT	GGTAAAACTT	TACGTCCCCA	CCACATACCA	AAGAGGCTGG	4380
AATTTAGCAT	GCTTTCTTCT	TTCAACTGTA	GGCAATGTGC	ACAAGTTCTA	AATCCTAAGA	4440
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CATCCAATGA	AGTTCTGACA	TTTCTTCAAC	ATGAGTACAG	TAATTCAATG	CCAGAGAATT	4560
CATTTTATTT	TGAAATCTAC	ATGCCATATT	CCAATTTCTG	TTGAAGATGC	AATGGTTATA	4620
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GCATTTGAGA	GGCTGAGGTG	GGCATATCAC	CTGAGGTCAG	GAGTTTGAGA	CCAGGCTGGC	4740
CAACATGGTG	AAACCCTGTC	TCTACTATAA	ATATAAAAAAT	TAGCTGGGTG	TGGTGGTGCA	4800
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GGTTGCAATG	AGTGGAAATC	GCACCAGTAC	ACTCCAGCCT	GGATGACAGA	GCAAAATAAT	4920



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TGATTCTCTT	GCCTCAGCCT	CCCAGTAGAC	TGGGACTACA	GGCGTGCACT	AGCATGCCCA	6180
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GGTGAACACC	GCCACACCTG	ACTAATTTGT	GTAGTTTTAT	TAGAGATGGG	GTTTCGCCAT	6420
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AGTGCTGGGA	TTACAGATGT	GAGACACCAG	ATCAGCCTCA	GAAGACATTT	TCTATTGGAA	6540
AGAGAAAACA	CTATTAGCAA	CCTATTAGTC	TAATATTTAA	TACTTAATGT	CTTCCTTAGT	6600

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TTATCAGTAT	TTGAATAAGA	GGGGGTCTAC	ATCTTAAGTA	CTGCTTAAGA	TGAAAGCCTC	6780
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TGTTATTGGA	GCCCAGAGAG	AAGAATTGAA	ATTCAAGTTT	TCTCTCTCTC	CTTTTCTCAC	6900
TCACCACAAT	AAGTCAGTTG	CACCAAGTCT	TGTAGCTCTT	TACTGAGCCA	TGTTTTTCACG	6960
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CAGAATCCAG	GAAAATAGGT	CTCTAGAAAT	TTGTCCATGG	TCCCAGATCT	CCATTTCTTG	8580
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AGTGGTAGGA	TTAGAGGGGT	GAGCAGAAAG	CAAAGGTTTT	TGAGTGGCCA	CAGGCCCCAC	8940
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TGATAGTACG	TAACTGACCT	ACTATTACAT	ACAAACAGAC	CAACCTTTAG	TAACAGCGCT	9420
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CATAAAAGCC	CTATAAGTAG	CAGAAATCCG	CTCTTTACTT	TCGACACATT	TCTGGTGTTT	10320
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CTGTTTTTCGT	GGCGCACACC	TTCGTAGTAT	ACTGAAGGGT	GTGTCTCCTG	GGTTTCCAAC	11280
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ACTGGTTTAT	TCAAGATTCA	AATCAAATCA	AATTTTGCTT	GAATCCCAGT	GCTCAGTCAG	11460
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AGACAAGTTT	GAAAGTTGCT	TTAGGAGAAG	CCAACTCTTA	ACTGCTGGGT	AAATTGACAA	11580
GCCTTCGAAC	ACTGAACTGA	AGGCCAGTAA	GGACTAGGCG	CTGGGTGGGG	GAGAATGAAG	11640

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ACAACTGCAG	GCCGCTTTGT	GGCCTGGGAA	ATTCCACATT	CCCTTAAGTA	TTTTACTCAT	11760
GGTCTTTTCC	AGGTAAAGAT	TTTAAGATGA	AGGGTTAGAC	GTAGTCTACC	TATCTTTTTA	11820
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CTTCAAGGGA	TCCTCCTGCC	TTGGTCTCAC	AAAATGCTGG	GATGACAGAC	ATGAGACACC	225480
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CACTTAGCAT	ACCCCTGGAC	AATGAAGTGT	TTTTTGTTTT	GTTTTTTTCAT	GTCCATCCTT	225900
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GCCTTTAGGT	ATTTTCACAC	TTGCTCTGTT	ACGTAAATGT	ATGTGTGTGT	GTGTGTGTGT	235020
GTGTGTGTGT	GTG					235033

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACACACACA CACACACACA CACACACACA CACAAATGAG GTATATAAAG GGTCTCCTAA	60
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CCAAAGTGCT	GGGATTACAG	GCAGGAGCCG	CCAGGGCTGC	CACTTTGATG	TCAGACTCAG	3000

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TCAAAGATGC	CCTGCAGAAC	TGTGTGGGAG	TCTCTCACAG	ATGGCTGCCT	GGGTGGGACC	3120
CCACCAAAC	GAAAGACCGA	GACTTCAGGC	AGGGCAGATG	GAGTAGGCCA	ACTACAGAGC	3180
CAGAGGTGAC	ACTGAGACAC	CACTGGGCCT	GGAAATCAGG	GCATCAAGCC	AAAGAGGGTT	3240
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ACCTTCCTTC	TTTCCTATTT	CTCCATTTTC	TAATGGGAAT	GTCTATTATG	CCTGTTTCAC	3360
CATTGTACCT	TAGAAGCATG	TAACATTTCT	GGTTTCACAC	GTTCAAAGCT	GGAAAGGAAT	3420
TTTGTCTCTG	GATGAATCAC	ACATTGAGCC	TCACCCGTAA	CCTGATTTAG	ATGATTTTTT	3480
AGATGACACT	TTGAACTTTA	GAATTGATGC	TAGAATGAGT	TAAGACTTTC	AGGGGGCTGT	3540
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GAGTGCAGTG	GCACCATCTT	GGCTCACTGC	AAGCTCTGCC	TCCCGGGTTT	ATGCCATTCT	3660
CATGTCTCAG	CCTCCAGAGT	AGCTGGGACT	ACAGGCGCCC	GCCACCACGC	CTGGCTAATT	3720
TTTTTTTTTAT	TTTAGTAGAG	ATGGGGTTTC	ACCGTGTTAG	CCAGAACGGT	CTCGATCTCT	3780
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CATGCCCCGC	TGGGATGGAA	TAAATTTATC	TTGTATGGGA	GAAGGACATA	CATTTTGGCA	3900
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATACA	AACACACAGT	GAGATGGCAG	4140
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CCTTTTCTCC	ATTATCTGTC	TTTCCAGTGA	TGAAATTTTG	ATCTGGCCCT	CCCAAGTATT	15660
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AAGCCAATTA	AATTCTTGGA	GACAATTTGT	ACTTTAAGGA	ATTCTTATAA	TATTTGTAAT	15960
TACCCTCATA	ACTTTTTTTT	TGCCCTACTT	CTGTGCTTCT	CTAATATGCA	GATTATTAAA	16020
TGTTGTTACA	AAGCCATTGT	CAAAAAAACA	AAAAACAAAA	AACTAAACAA	ACTCACATGG	16080
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GCCAGAAATC	GTGAAGACAT	GGCCTACCTA	ACTTGGAAT	GTTGGTTGTC	AGTGGAAT	16200
ACTACACAGA	GATAGCCATA	GTGCTGCACA	GCCAATCTTA	AGTGTTTCTA	GAGAATCACT	16260
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GAGTATCCAT	ACTAACTCT	TTTCTACTGA	AAATAATGTG	CAAACATAAC	ATCCTATTCC	16380
TAGACAGTTT	GTAGTTTTTT	TCTCCCATTT	CTATTTTATA	AATCATCTTT	TTAAAATACT	16440

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GTAATAATTG	CCCTACTCAT	AAAGATGGGG	TGAAGATTAA	ATGAAATAGC	ACCTATAGAA	16620
CACTAGTTCC	AGACGTGGTA	TCATGCTAGT	AAAATGGCTG	CACAGCACTG	CTCAATGATG	16680
ACAAAAAGTG	AAGCTTCTGG	AGACAGACTC	CAAGTTTGAC	TCCCAGATCA	CCACATATAA	16740
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GCTCCTAAAA	GGACTTGAAG	CAGCTTATGA	CTGAAGACTT	TGGTAGGAGT	TGGCCTTCTA	16980
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GATCTCCTTG	CTGCTGGCTC	AGAAGGGTAA	AAGAGCAGAA	ATGATGGGGC	TTCTCTCATT	18000
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AGCTTTC AAC TGTTTTGAAA TCACTTTCAG GGTGGTCATG TAGTTGCTTT TTTGAAATCA 231060  
GAAGATGATT CTGCCTCTTT TAATATGTGA CTCCTCAGAT TCAGAAAGTG CTCGCTAGTC 231120  
TTAAGAGTGA ATTACCCTCA GTGGTCCAGC GCTTATGAAC CCACATCTAA CCCTATCCCC 231180  
TGGGGGAACT ATCAGAGAAA TTGGTGCCAT GGACATAAGA GGAAGGCACA GTGAAGCAGA 231240  
GAGCCCCGCA TGATGAAAAT CAGTGGACAG CATCATTATT TACAACCTTG TAATCACCCA 231300  
GGAGCATGAA AATCCAGGCC AATCTGGCAC CATGAGCTCT AATTTTTGTT GGAGTTCTTG 231360  
GAACCGATT TCATGAATGA CTGTTTAGCC ATTTTAGAGT GTGGCATACT TGGCTGCTGG 231420  
CATACAGAGG TTGGATGTAA ACGGGCCTTT GCCCTCTCTT ATGAACATAG ACAGGAAC 231480

AACTGTGTCA CATAGGTTCC AAATGGTGGC CTGAATACTA TTTACAATA AGGTACAATG 231540  
 AAATTGAGTA AGTCTTTTCC TCTTTTGCAG ATACCATCAT TATTCATATA TTTCTTCAAA 231600  
 GTTAACTATT TGTATTTGGT AATTTTAAAT AGAAATGTAA TAATTGCTTC TCAAGTTTAG 231660  
 TCTTTAGTCT TAAGGTTGAT GCTCTCCATG TCCTTCCAAA AAAAGGTATG TTGCTTTTAT 231720  
 TATATCCTCG CCTTCAGATG GGATTATTCC ATTTTGTTC TTTGTTAATAT ATACTTTGAG 231780  
 CCACTTTTTT TGTGGCTCTG GGTGAGATGC TATAGGTACA ATGACAAGTG ATACGTGTGT 231840  
 TGTCCCTGTC ACAAAAGTGG ATAGCCTAAG TGGTGACTTT TACCTCCACT CCAAATATAT 231900  
 GTATCACACA CCAGCCGTAT GCCAGGCACC ACTCTAGGTG CTAGGGATAC AGCAGTAAAC 231960  
 AGACAAATGC AACCCTGCC CATGTGAAAG AGAATAAGAC AATAAATAAG TAAAGTGCAT 232020  
 GTTATATGGA GGTGGCAAAT GCTAAAAAGA AAAATTAAGC AGGCAAGAGG ACTCATTGAA 232080  
 AAGATGACAT TTGGGTAAAA GCCCATGTAT ATATGTTCTA TTGGTTTTAT TTCTCTGGAG 232140  
 AGCCCTGACT AATACACAAT GACTTTGAGA AGTTACTGGC TTTTGATTTA TCACACTATT 232200  
 CGGAGTGCTG AGAGCCTTCT TAGTGTGTAT TCAGTGTTTT AAGAGAGCTT GTGGATGAAT 232260  
 AATAAATAGG ACAAATTTA TCCAACTTA AGCCTTGCTT TAGGTAAAAG GGCTCCTCTT 232320  
 ACAAGGTAGA AGGTTATTAT TTGACATTTA AATCCAAC TG AAGACTAATA AGACTAATTA 232380  
 ATTAAAAGTT TTTAAATCAC AACTGCGTGC AAAATAAATG GAACTGCCAT GCTCGCCAAG 232440  
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 GCTCCATTTT TCTCCTAAAA TCAGTAAGAC AGAAGCTGGT CAGATTATCA AGAGCCCTAG 232560  
 TTAAACACAG CAGTAGCATT TGGAAGGGGT TGCTCTCAT T AGGCAGTGCC TGACCACAAC 232620  
 AAGAGATGAA CAAGCCCTGT ATCTGAAGCC ATCATGCCTA GTTATGGTCC CCGACTGTTC 232680  
 ATGATGCCTG GAAGGGAGGC CCCCTGCACC CTAGAAAGCT GGGTGGGTTC TACTGTCTGC 232740  
 TTTACTGCTA AAAACCCTCT TCTTTGGATC TGGACTTTAC CTCTATCTGA TTTTTTTTTT 232800  
 TAATATATGA TTTGGCACTG AGTCTGTCAC TGCTGCTAAC TCAGCAGTTC TAGGGTCATT 232860  
 GCCCCATTGC CTCACAGAAA GAATTTTATA GCTTCCAGCA TCCTCTCTCC TTCATTATAC 232920  
 TTTGATTTCA GCATTGCTAT TTTTCTCTT GGGTGTGCA GCTCTCTCTC TCCTTCCCAT 232980  
 GTCTTGTTGG TTTTCTGCTA ACTCCTGCTT TTTTCTTTT TTTTTTTTTG AGACGGAGTC 233040  
 TCGTTCTGTC ACCCAGGCTG GAGTGCAGTG GCACAATCTC GGCTCACTGC AACCTCCGCC 233100  
 TCCCGGGTTC AAGCTATTCT CCTGCCTCAG CCTCCCAAGT AGCTGGGACT ACAGGCGCTC 233160

ACCACTATGC CCCACTAATT TTTGTATTTT TAGTATTGCT GTCATCAATC CACATGTCCA 233220  
 GAAGCACCTA GAAACTCTAA TTCTTTGTAG GTATCAAACC CTAGGACTCT TTCCTCTAAT 233280  
 CACAATATAT AATCCCTGAT TCCCAAACAC GGTCTTTTCA TATACATTTT CCACTGTACA 233340  
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 TTATTTGTTT TATCTGAATG TAATCTCCCA GAGGGTGTTA TCATCTTTTT TTTTGAGATG 233520  
 GAGTCTTGCT TTGCTGCCCC GGCTGGAGTG CAGTGGCATG ATCTCGGCTC ACAGCAACCT 233580  
 CCACCTCCTG GGTTCAGTG ATTCTCCTGC CTCAGCCTCC TGAGTAGCTG GGATTACAGA 233640  
 CGTGTGTCAC CACACCTGGC TAATTTTTGT ATTTTGTAGT GAGACAGGGT TTCACCGTGT 233700  
 TGGCAAGGCT TTCCTCGAAC TCCCAAATC AGGTGATCCA CCCACCTCAG CCTCCCAAAG 233760  
 TGCTGGGATT ACAGGTGTGA GCCACCATGT CCAGCCCCAT CTTTTCTTT TAGTTTAGTT 233820  
 CTTAACAAAT AGTCTGACAC AAAGTGGATA TAACAATATT TTGAATTATG AATAACTAAA 233880  
 TGAATATTTT CAGATTCCT GGTGCTCTCA AAGTTTTATG TTACAAAAGA AAAACAAGTC 233940  
 TAAAATACCT GCCTCAAGTT TTTATCTGTA CTATGATTTT AAACCAAATA AAAAACAGGT 234000  
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 AATACTAGGT CATTTTTCTT GTTTCCCCAA CTTCATTTT TATAGCAATA AAAAGAAACA 234120  
 AGTAAATGTA TGTTAATTTA ATTTAAAAGA AGTAGTCTAC CATCTCTTCT GTTAAAAAGA 234180  
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 TTTGTCTATC TGTTAGCTTT TTATTATTTT CTTTGTAGG TTTGAATTTT AAACCACATA 234360  
 AATCTGTTAC ATGCTCATAA TAATAAGTTT AAAATAAAAC TTTTGGCTGG GTGCAATGAC 234420  
 TTACACCTGT AATCCAGCG CTTTGGGAAG CAGAGGTGGG AGGATACTTG AGGCCAGGAA 234480  
 TTTGAGATCA GCCTGGGCAA CATAGTGAGA CCCTGCCTCT GTAGAAATAA ACAAAAATTA 234540  
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 GGGCAATAAG GTGAGAACTT GTCTCAAAAA AAAAAGGGGG GGGGGAAACA AATAAATAAA 234720  
 TATAACAAA ACTTTTGT TTCAAATATGT AATATTTAGC ACTAAAGAAT TCTGAATTGT 234780  
 AGAGCTAAAA AGTACTTAAA AGTTAATAAC TATTGTCTCC TTTAAAAGAA TTGTTATCAA 234840

AGTATAATTT TTATCCAGAA AATCATCCAT ATCAGCAAGC TAAACTTTCT CAAAATGACA 234900  
 TATCCATGTA ATTAGCTCCC AGGTAATTAG CAGGCAGCCT CTA CTCAGGT TGAGTATTCC 234960  
 TAATCTAAAA ATTGGAAATT CAAAATGCTC CAAAATCTGC AACTTTTTGA ATGCTAACAT 235020  
 GATTCTCAAA GGAGTGCTCA TGGAGTATTT CAGATTTTGG ATTTTGGAT TTGAGATACT 235080  
 CAGTATAATG CAAACATTCC AAATCTGAAA AAATCTGAAA TACTTCTGGT TCTAAGCATA 235140  
 AGGGATACTC AACGTGTGTT AGCTAATTAG ACCCTTCATG GTCTCTTCTA GACCTCAGCT 235200  
 TCTTCAAGGT AACCTCTATC CTCACTTCTA ATAGCATGAA CTTTTCTGTT TTAGAATAAT 235260  
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 TTCTTGCTTT TCATGACCTT AACAGTCCTG AAGATCATTT GCTTTTTTTT CATAATTACA 235620  
 CCGGAGTTAT AGATTTTTTG AAATAATACC ACAAGGGCAA AGGGCCCTTC TTGTCACATC 235680  
 ATTTTAGGGA GAACATGATA TCCACATGAC ATCACTGATA TTAACCTTCA TCATGTGGTT 235740  
 TAGGTAATGT TTCAGGTTTC TCTACTGCAA AGTGATTTTT TTCCCTTAAT TTAGCCCACC 235800  
 TGAACCTATC AATTTTGTTT TCTTCCATGA CTAATACTTT TGTTATTATA GCTAAACTT 235860  
 CATTTGGGCC AAATCTTAGA TCATGTAAAT TTTCTTCTAT ATTTTATTCT AAAAGCTTGT 235920  
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 ATTTTtaggt ACTTTTGTAT AAGGTGTGAG AGATGTCTCC AGTTTCACTT TATTAACACA 236040  
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 GTTTGTGAGC GTGTTTCTGG ATGAGATTAG CCTTTGAATA GGTGATCCTA GTAAAGTAAA 236340  
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 AAGGCAGAGG AAGGGGAAT TTGGGCCTTT TTTTCTGCCT CACTGCTTGA GCTGGGACAT 236460  
 CTCATCTGGT CTCCTGCTCT TGAAGTGGGA TTTACATCAT CAGTTCCTCT GGTTCTCAGG 236520

CCTTCAGATT CAGACTGAAT CATACCACCA GCTTTCCTGG GTCTCCAGCT TGCAGATTAC 236580  
 AGATCATGGG ACTCCTCATC TTCCATAAAT GCATGAGCCA ATTCAGTCTA TGTCCCTGAA 236640  
 AACTGCCCCA CTGCAGATTA AGGCTTTTTT CCACTAGGTG AAATAAGAA GCTTGTTAGA 236700  
 CAGATTTCCC TTCATCCAGT GCCCTCTCCT CTTTAAGTTA CAACACATTG GCTACACCTA 236760  
 AGTGCAGGGG TGGGGATGAG GGTATAGTCC TCTTGTTTGC TGAGAAGAGA ACTGTATTGG 236820  
 GAAAGCTCTA GAAGTGTTTG ATACATACAT AAACAAGGCA TGGTTTTTGC ACTTAATTTT 236880  
 ACATTACATT TTTCCAGAA AAAAAGGAAT GTATAGGCAT CACGTAAGT TACTAGCTGG 236940  
 AGTCATTCTT CCTGATTATC AAAGGTAAAC AGTTATTAAT CCTATACCA GATGTCAAGG 237000  
 AGAAGTACTT TTGGAACACA AGGAATTCTC TGGGAGTCCT TACTACTCTC AAGCCCAGTG 237060  
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 ATTTAGGAAT TTGCCTTACC AAGTAAAACA TAAGGGCAGC TGAGGTGCTG ACTGAAGACA 237180  
 AATGGAGCAT AGAATAAGAG TAGTAAAGAA TGCCAAAAAT GCTGTCATGT ATCCATTGAC 237240  
 AAAAGGAGCT ATAAAGCCTT TAGGTATTTT CACACTTGCT CTGTTACGTA AATGTATGTG 237300  
 TGTGTGTGTG TGTGTGTGTG TGTGTG 237326

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTTAGAACG CGGCTACAAT

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCGATTCAT TAATGCAGGT 20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTAAAACG ACGGCCAGTC 20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCAGGAAACA GCTATGACC 19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCATCAGCGA TTAATTCTA C 21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGCATTGTG GTGAAATCAG GG

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGAGTAATT GTTTAAGGTG C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGAGTAATT GTTTAAGGTG T

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGAAGAGATA GATATGGTGG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATGTGACC GTCCCATGAG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAACTGAATA TGCAGAAAAA AGTACACC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTAGCTGGG ACTCACGGTG T

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTAGCTGGG ACTCACGGTG C

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGCCACCAC TCCCAGCTCA T

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCACACACCG ATTGG

15

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAACTGAT CTTTGA

16

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATATATATA TATA

14

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAAAAAAAAA AAAA

14

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGGATGGTCT

10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGTTGTTGT TG

12

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTTTTTTTTT TTTT

14

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATAATAATA AT

12

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTTTTTTT T

11

2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATATATATAT ATATATATAT

20